

1 GGCACGAGGT CCCCACGCG CCCCGCCAA CCCCTACGAT GAAGAGGGCG 50  
1 M K R A 4  
51 TCCGCTGGAG GGAGCCGGCT GCTGGCATGG GTGCTGTGGC TGCAGGCCTG 100  
5 S A G G S R L L A W V L W L Q A W 21  
101 GCAGGTGGCA GCCCCATGCC CAGGTGCCTG CGTATGCTAC AATGAGCCCA 150  
22 Q V A A P C P G A C V C Y N E P K 38  
151 AGGTGACGAC AAGCTGCCCC CAGCAGGGCC TGCAGGCTGT GCCCGTGGGC 200  
39 V T T S C P Q Q G L Q A V P V G 54  
201 ATCCCTGCTG CCAGCCAGCG CATCTTCCTG CACGGCAACC GCATCTCGCA 250  
55 I P A A S Q R I F L H G N R I S H 71  
251 TGTGCCAGCT GCCAGCTTCC GTGCCTGCCG CAACCTCACC ATCCTGTGGC 300  
72 V P A A S F R A C R N L T I L W L 88  
301 TGCACTCGAA TGTGCTGGCC CGAATTGATG CGGCTGCCTT CACTGGCCTG 350  
89 H S N V L A R I D A A A F T G L 104  
351 GCCCTCCTGG AGCAGCTGGA CCTCAGCGAT AATGCACAGC TCCGGTCTGT 400  
105 A L L E Q L D L S D N A Q L R S V 121  
401 GGACCCTGCC ACATTCCACG GCCTGGGCCG CCTACACACG CTGCACCTGG 450  
122 D P A T F H G L G R L H T L H L D 138  
451 ACCGCTGCGG CCTGCAGGAG CTGGGCCCCG GGCTGTTCCG CGGCCTGGCT 500  
139 R C G L Q E L G P G L F R G L A 154  
501 GCCCTGCAGT ACCTCTACCT GCAGGACAAC GCGCTGCAGG CACTGCCTGA 550  
155 A L Q Y L Y L Q D N A L Q A L P D 171  
551 TGACACCTTC CGCGACCTGG GCAACCTCAC ACACCTCTTC CTGCACGGCA 600  
172 D T F R D L G N L T H L F L H G N 188

FIG. 1A

601 ACCGCATCTC CAGCGTGCCC GAGCGCGCCT TCCGTGGGCT GCACAGCCTC 650  
 189 R I S S V P E R A F R G L H S L 204

651 GACCGTCTCC TACTGCACCA GAACCGCGTG GCCCATGTGC ACCCGCATGC 700  
 205 D R L L L H Q N R V A H V H P H A 221

701 CTTCCGTGAC CTTGGCCGCC TCATGACACT CTATCTGTTT GCCAACAATC 750  
 222 F R D L G R L M T L Y L F A N N L 238

751 TATCAGCGCT GCCCACTGAG GCCCTGGCCC CCCTGCGTGC CCTGCAGTAC 800  
 239 S A L P T E A L A P L R A L Q Y 254

801 CTGAGGCTCA ACGACAACCC CTGGGTGTGT GACTGCCGGG CACGCCCACT 850  
 255 L R L N D N P W V C D C R A R P L 271

851 CTGGGCCTGG CTGCAGAAGT TCCGCGGCTC CTCCTCCGAG GTGCCCTGCA 900  
 272 W A W L Q K F R G S S S E V P C S 288

901 GCCTCCCGCA ACGCCTGGCT GGCCGTGACC TCAAACGCCT AGCTGCCAAT 950  
 289 L P Q R L A G R D L K R L A A N 304

951 GACCTGCAGG GCTGCGCTGT GGCCACCGGC CCTTACCATC CCATCTGGAC 1000  
 305 D L Q G C A V A T G P Y H P I W T 321

1001 CGGCAGGGCC ACCGATGAGG AGCCGCTGGG GCTTCCCAAG TGCTGCCAGC 1050  
 322 G R A T D E E P L G L P K C C Q P 338

1051 CAGATGCCGC TGACAAGGCC TCAGTACTGG AGCCTGGAAG ACCAGCTTCG 1100  
 339 D A A D K A S V L E P G R P A S 354

1101 GCAGGCAATG CGCTGAAGGG ACGCGTGCCG CCCGGTGACA GCCCGCCGGG 1150  
 355 A G N A L K G R V P P G D S P P G 371

1151 CAACGGCTCT GGCCACGGC ACATCAATGA CTCACCCTTT GGGACTCTGC 1200  
 372 N G S G P R H I N D S P F G T L P 388

FIG. 1B

1201 CTGGCTCTGC TGAGCCCCCG GCTCACTGCA GTGCGGCCCC AGGGCTCCGA 1250  
 389 G S A E P P A H C S A A R G L R 404  
 1251 GCCACCAGGT TCCCCACTTC GGGCCCTCGC CGGAGGCCAG GCTGTTCACG 1300  
 405 A T R F P T S G P R R R P G C S R 421  
 1301 CAAGAACCGC ACCCGCAGCC ACTGCCGTCT GGGCCAGGCA GGCAGCGGGG 1350  
 422 K N R T R S H C R L G Q A G S G G 438  
 1351 GTGGCGGGAC TGGTGA CTCA GAAGGCTCAG GTGCCCTACC CAGCCTCACC 1400  
 439 G G T G D S E G S G A L P S L T 454  
 1401 TGCAGCCTCA CCCCCCTGGG CCTGGCGCTG GTGCTGTGGA CAGTGCTTGG 1450  
 455 C S L T P L G L A L V L W T V L G 471  
 1451 GCCCTGCTGA CCCCCAGCGG ACACAAGAGC GTGCTCAGCA GCCAGGTGTG 1500  
 472 P C \* 473  
 1501 TGTACATACG GGGTCTCTCT CCACGCCGCC AAGCCAGCCG GGCGGCCGAC 1550  
 1551 CCGTGGGGCA GGCCAGGCCA GGTCTCCCT GATGGACGCC TGCCGCCCCG 1600  
 1601 CACCCCCATC TCCACCCCAT CATGTTTACA GGGTTCGGCG GCAGCGTTTG 1650  
 1651 TTCCAGAACG CCGCCTCCCA CCCAGATCGC GGTATATAGA GATATGCATT 1700  
 1701 TTATTTTACT TGTGTAAAAA TATCGGACGA CGTGAATAA AGAGCTCTTT 1750  
 1751 TCTTAAAAAA AAAAAAAAAA AACTCGA 1777

FIG. 1C

202109090909

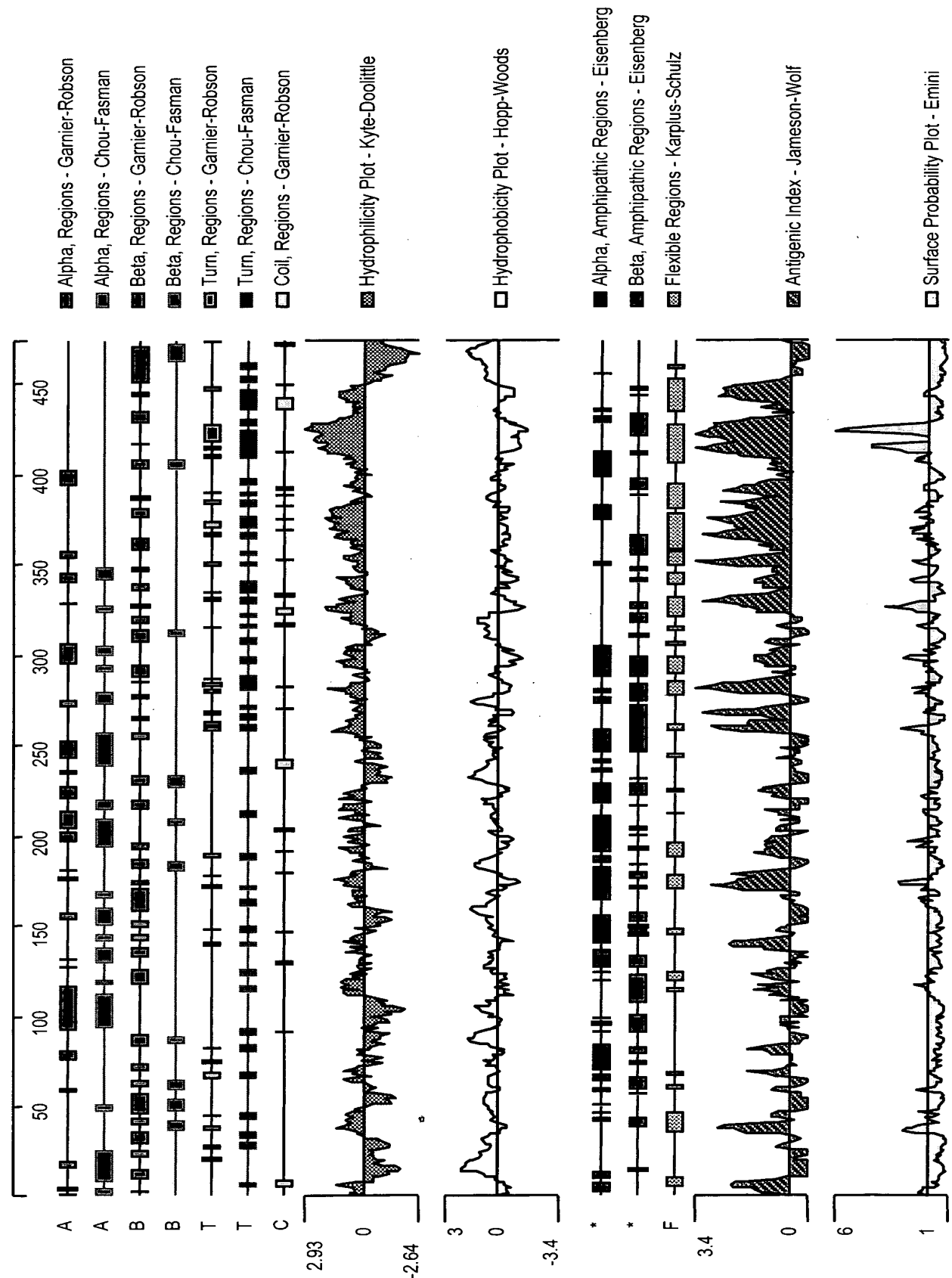


FIG. 2